

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 16, 2003, 13:58:46 ; Search time 77 Seconds
(without alignments)
58.871 Million cell updates/sec

Title: US-09-914-213-2

Perfect score: 116
Sequence: 1 GLEISEINEDIKCEFPDME 22

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	116	100.0	996	4 Q99989	Q99989 homo sapien
2	116	100.0	1481	6 Q9TU02	Q9TU02 macaca neme
3	116	100.0	1481	6 Q9TSP5	Q9TSP5 papio anubi
4	116	100.0	1481	6 O62573	O62573 macaca mula
5	110	94.8	1481	6 O62568	O62568 macaca mula
6	103	88.8	1481	6 Q9TXX9	Q9TXX9 oryctolagus
7	95	81.9	1466	13 Q98TR8	Q98TR8 bufo bufo (
8	91	78.4	1485	13 P70034	P70034 xenopus lae
9	77	66.4	1503	13 O73677	O73677 fundulus he
10	68	58.6	235	6 O8SPT1	O8SPT1 pan troglod
11	67	57.8	1518	13 Q9TAR8	Q9TAR8 salmo salar
12	64	55.2	1490	13 Q98TYS	Q98TYS salmo salar
13	64	55.2	1519	13 Q9W750	Q9W750 salmo salar
14	62	53.4	1511	13 Q918E2	Q918E2 fuqu rubrip
15	56	48.3	244	13 Q9DDK8	Q9DDK8 neoturus ma
16	55	47.4	805	13 Q918A9	Q918A9 xenopus lae

17	52	44.8	499	17 Q8U3L0	Q8U3L0 pyrococcus
18	51	44.0	50	2 Q06970	Q06970 bacillus su
19	51	44.0	705	16 Q99UK3	Q99UK3 staphylococ
20	50	43.1	205	5 P90631	P90631 euploies cr
21	50	43.1	682	5 Q9N9B8	Q9N9B8 leishmania
22	49	42.2	260	16 Q931M4	Q931M4 staphylococ
23	49	42.2	1680	4 Q9P129	Q9P129 homo sapien
24	48	41.4	154	10 Q9ZR02	Q9ZR02 arabidopsis
25	48	41.4	413	17 Q28445	Q28445 archaeoglob
26	48	41.4	558	16 Q8RH60	Q8RH60 fusobacteri
27	48	41.4	893	4 Q9N212	Q9N212 homo sapien
28	48	41.4	1016	5 Q92585	Q92585 homo sapien
29	48	41.4	1087	4 Q96923	Q96923 dictyostell
30	48	41.4	1928	5 Q9U0H2	Q9U0H2 plasmodium
31	47.5	40.9	230	12 Q9YVZ1	Q9YVZ1 melanoplus
32	47.5	40.9	414	11 Q9DBC1	Q9DBC1 mus musculu
33	47.5	40.9	414	11 Q8R588	Q8R588 mus musculu
34	47	40.5	930	10 Q9FMN2	Q9FMN2 arabidopsis
35	47	40.5	1002	10 Q94KS1	Q94KS1 arabidopsis
36	47	40.5	1048	10 Q9LRA8	Q9LRA8 arabidopsis
37	46.5	40.1	235	16 Q31789	Q31789 bacillus su
38	46.5	40.1	319	10 Q9SK30	Q9SK30 arabidopsis
39	46.5	40.1	338	15 Q91UB9	Q91UB9 human immun
40	46.5	40.1	380	2 Q9X3R3	Q9X3R3 pseudomonas
41	46.5	40.1	903	3 Q9HGM1	Q9HGM1 schizosacch
42	46	39.7	104	16 Q9CR37	Q9CR37 lactococcus
43	46	39.7	232	16 Q9PNS4	Q9PNS4 staphylococ
44	46	39.7	244	10 Q9SRD6	Q9SRD6 arabidopsis
45	46	39.7	304	5 Q16680	Q16680 caenorhabdl

ALIGNMENTS

RESULT 1
Q99989 PRELIMINARY; PRT; 996 AA.
ID Q99989
AC Q99989;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transmembrane chloride conductor protein (Fragment).
GN CCTR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Scheet, P, Maggi, L, Blandford M.;
RT "The sequence of H. sapiens BAC clone 068P20.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC000111; AAB46352.1; -
DR HSSP: P13569; 1NBD.
DR InterPro: IPR001140; ABCtransprtTM.
DR InterPro: IPR003439; ABC_transprt.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran; 1.
DR ProDom: PD000006; ABC_transport; 1.
DR TRGFAMS: TIGR01271; CCTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
FT NON_TER 996
SQ SEQUENCE 996 AA; 113334 MW; 0F85321034CA8DBF CRC64;

Query Match 100.0%; Score 116; DB 4; Length 996;
Best Local Similarity 100.0%; Pred. No. 4,6e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLEISEINEDIKCEFPDME 22

DB 817 GLEISEINEEDLKECFDDME 838

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RESULT 2
O9TU02 PRELIMINARY: PRT: 1481 AA.
AC O9TU02:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2002 (TREMBlrel. 13, Last sequence update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Wine J.J., Kuo E., Hurllock G., Glavac D., Dean M.;
RT "CFTR genomic sequences from five primate species.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162400; AAD46905.1; JOINED.
DR EMBL: AF162374; AAD46905.1; JOINED.
DR EMBL: AF162375; AAD46905.1; JOINED.
DR EMBL: AF162376; AAD46905.1; JOINED.
DR EMBL: AF162377; AAD46905.1; JOINED.
DR EMBL: AF162378; AAD46905.1; JOINED.
DR EMBL: AF162379; AAD46905.1; JOINED.
DR EMBL: AF162380; AAD46905.1; JOINED.
DR EMBL: AF162381; AAD46905.1; JOINED.
DR EMBL: AF162382; AAD46905.1; JOINED.
DR EMBL: AF162383; AAD46905.1; JOINED.
DR EMBL: AF162384; AAD46905.1; JOINED.
DR EMBL: AF162385; AAD46905.1; JOINED.
DR EMBL: AF162386; AAD46905.1; JOINED.
DR EMBL: AF162387; AAD46905.1; JOINED.
DR EMBL: AF162388; AAD46905.1; JOINED.
DR EMBL: AF162389; AAD46905.1; JOINED.
DR EMBL: AF162390; AAD46905.1; JOINED.
DR EMBL: AF162391; AAD46905.1; JOINED.
DR EMBL: AF162392; AAD46905.1; JOINED.
DR EMBL: AF162393; AAD46905.1; JOINED.
DR EMBL: AF162394; AAD46905.1; JOINED.
DR EMBL: AF162395; AAD46905.1; JOINED.
DR EMBL: AF162396; AAD46905.1; JOINED.
DR EMBL: AF162397; AAD46905.1; JOINED.
DR EMBL: AF162398; AAD46905.1; JOINED.
DR EMBL: AF162399; AAD46905.1; JOINED.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABC_transporter.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR005291; CAMP_channel.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran_2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFRAMS: TIGR00953; 3a01202; 1.
DR TIGRFRAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA: 168460 MW: A9AE0CC87E267570 CRC64;
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Query Match 100.0%; Score 116; DB 6; Length 1481;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEEDLKECFDDME 22
DB 817 GLEISEINEEDLKECFDDME 838

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RESULT 3
O9TSP5 PRELIMINARY: PRT: 1481 AA.
AC O9TSP5:
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-JUN-2002 (TREMBlrel. 13, Last sequence update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Papio anubis (Olive baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Papio.
OX NCBI_TaxID=9555;
RN [1]
RP SEQUENCE FROM N.A.
RA Wine J.J., Kuo E., Hurllock G., Glavac D., Dean M.;
RT "CFTR genomic sequences from five primate species.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF162401; AAD46907.1; JOINED.
DR EMBL: AF162401; AAD46907.1; JOINED.
DR EMBL: AF162402; AAD46907.1; JOINED.
DR EMBL: AF162403; AAD46907.1; JOINED.
DR EMBL: AF162404; AAD46907.1; JOINED.
DR EMBL: AF162405; AAD46907.1; JOINED.
DR EMBL: AF162406; AAD46907.1; JOINED.
DR EMBL: AF162407; AAD46907.1; JOINED.
DR EMBL: AF162408; AAD46907.1; JOINED.
DR EMBL: AF162409; AAD46907.1; JOINED.
DR EMBL: AF162410; AAD46907.1; JOINED.
DR EMBL: AF162411; AAD46907.1; JOINED.
DR EMBL: AF162412; AAD46907.1; JOINED.
DR EMBL: AF162413; AAD46907.1; JOINED.
DR EMBL: AF162414; AAD46907.1; JOINED.
DR EMBL: AF162415; AAD46907.1; JOINED.
DR EMBL: AF162416; AAD46907.1; JOINED.
DR EMBL: AF162417; AAD46907.1; JOINED.
DR EMBL: AF162418; AAD46907.1; JOINED.
DR EMBL: AF162419; AAD46907.1; JOINED.
DR EMBL: AF162420; AAD46907.1; JOINED.
DR EMBL: AF162421; AAD46907.1; JOINED.
DR EMBL: AF162422; AAD46907.1; JOINED.
DR EMBL: AF162423; AAD46907.1; JOINED.
DR EMBL: AF162424; AAD46907.1; JOINED.
DR EMBL: AF162425; AAD46907.1; JOINED.
DR EMBL: AF162426; AAD46907.1; JOINED.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABC_transporter.
DR InterPro: IPR003439; ABC_transporter.
DR InterPro: IPR005291; CAMP_channel.
DR Pfam: PF00664; ABC_membrane_2.
DR Pfam: PF00005; ABC_tran_2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFRAMS: TIGR00953; 3a01202; 1.
DR TIGRFRAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA: 168474 MW: A9AE0F3BB4192570 CRC64;
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Query Match 100.0%; Score 116; DB 6; Length 1481;
Best Local Similarity 100.0%; Pred. No. 6.8e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEEDLKECFDDME 22
DB 817 GLEISEINEEDLKECFDDME 838

RESULT 4
062673

DR	EMBL:	AF162357;	AAD46904.1;	JOINED.
DR	EMBL:	AF162358;	AAD46904.1;	JOINED.
DR	EMBL:	AF162359;	AAD46904.1;	JOINED.
DR	EMBL:	AF162360;	AAD46904.1;	JOINED.
DR	EMBL:	AF162361;	AAD46904.1;	JOINED.
DR	EMBL:	AF162362;	AAD46904.1;	JOINED.
DR	EMBL:	AF162363;	AAD46904.1;	JOINED.
DR	EMBL:	AF162364;	AAD46904.1;	JOINED.
DR	EMBL:	AF162365;	AAD46904.1;	JOINED.
DR	EMBL:	AF162366;	AAD46904.1;	JOINED.
DR	EMBL:	AF162367;	AAD46904.1;	JOINED.
DR	EMBL:	AF162368;	AAD46904.1;	JOINED.
DR	EMBL:	AF162369;	AAD46904.1;	JOINED.
DR	EMBL:	AF162370;	AAD46904.1;	JOINED.
DR	EMBL:	AF162371;	AAD46904.1;	JOINED.
DR	EMBL:	AF162372;	AAD46904.1;	JOINED.
DR	EMBL:	AF162177;	AAF80467.1;	-
DR	EMBL:	AF162151;	AAF80467.1;	JOINED.
DR	EMBL:	AF162152;	AAF80467.1;	JOINED.
DR	EMBL:	AF162153;	AAF80467.1;	JOINED.
DR	EMBL:	AF162154;	AAF80467.1;	JOINED.
DR	EMBL:	AF162155;	AAF80467.1;	JOINED.
DR	EMBL:	AF162156;	AAF80467.1;	JOINED.
DR	EMBL:	AF162157;	AAF80467.1;	JOINED.
DR	EMBL:	AF162158;	AAF80467.1;	JOINED.
DR	EMBL:	AF162159;	AAF80467.1;	JOINED.
DR	EMBL:	AF162160;	AAF80467.1;	JOINED.
DR	EMBL:	AF162161;	AAF80467.1;	JOINED.
DR	EMBL:	AF162162;	AAF80467.1;	JOINED.
DR	EMBL:	AF162163;	AAF80467.1;	JOINED.
DR	EMBL:	AF162164;	AAF80467.1;	JOINED.
DR	EMBL:	AF162165;	AAF80467.1;	JOINED.
DR	EMBL:	AF162166;	AAF80467.1;	JOINED.
DR	EMBL:	AF162167;	AAF80467.1;	JOINED.
DR	EMBL:	AF162168;	AAF80467.1;	JOINED.
DR	EMBL:	AF162169;	AAF80467.1;	JOINED.
DR	EMBL:	AF162170;	AAF80467.1;	JOINED.
DR	EMBL:	AF162171;	AAF80467.1;	JOINED.
DR	EMBL:	AF162172;	AAF80467.1;	JOINED.
DR	EMBL:	AF162173;	AAF80467.1;	JOINED.
DR	EMBL:	AF162174;	AAF80467.1;	JOINED.
DR	EMBL:	AF162175;	AAF80467.1;	JOINED.
DR	HSSP:	PI3569;	INBD.	
DR	InterPro:	IPR003593;	AAA_Appase.	
DR	InterPro:	IPR001140;	ABCtransprtm.	
DR	InterPro:	IPR003439;	ABC transprtm.	
DR	InterPro:	IPR005291;	CAMP_cl_channel.	
DR	Pfam:	PF00664;	ABC_tran; 2.	
DR	Pfam:	PF00003;	ABC_tran; 2.	
DR	ProDom:	PDO00006;	ABC_transportr; 2.	
DR	SMART:	SM00382;	AAA; 1.	
DR	TIGRFAMS:	TIGR00953;	3a01202; 1.	
DR	TIGRFAMS:	TIGR01271;	Cfmr_protein; 1.	
DR	PROSITE:	PS00211;	ABC_TRANSPORTER; UNKNOWN_1.	
KW	ATP-binding;	Transmembrane.		
SQ	SEQUENCE	1481 AA;	168487 MW; A9AE0F3BB1197570 CRC64;	
Query Match				
Best Local Similarity 100.0%; Score 116; DB 6; Length 1481;				
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1	GLEISEEINEDLKRCFPDME	22	
DB	817	GLEISEEINEDLKRCFPDME	838	
RESULT 5				
ID	062668	PRELIMINARY;	PRT;	1481 AA.
AC	062668;			
DT	01-AUG-1998	(TREMBLrel. 07, Created)		
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)		

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DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update).
OC Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecidae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98191731; PubMed=9530627;
RA Wine J.J., Glavac D., Hurlock G., Robinson C., Lee M., Potocnik U.,
RT "Genomic DNA sequence of Rhesus (M. mulatta) cystic fibrosis (CFTR)
RT gene."
RL Mamm. Genome 9:301-305(1998).
DR EMBL: AF013753; AAC14011.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF03005; ABC_transportr; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA; 168454 MW; 9D204B89F37B7699 CRC64;

Query Match          94.8%; Score 110; DB 6; Length 1481;
Best Local Similarity 95.5%; Pred. No. 4.8e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEDLKECFDDME 22
DB 817 GLEISEINEDLKECFDDME 838

RESULT 6
Q9TXX9 PRELIMINARY; PRT; 1481 AA.
AC Q9TXX9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Chloride channel.
GN CFTR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BREED NEW ZEALAND WHITE; TISSUE=CORNEA;
RA Rae J.L.;
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF189720; AAF01067.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR InterPro: IPR003439; ABC_transportr.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1481 AA; 168454 MW; 9D204B89F37B7699 CRC64;

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KW ATP-binding.
SQ SEQUENCE 1481 AA; 168041 MW; 1B217AAE75DDE8A CRC64;

Query Match          88.8%; Score 103; DB 6; Length 1481;
Best Local Similarity 86.4%; Pred. No. 4.7e-06;
Matches 19; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GLEISEINEDLKECFDDME 22
DB 817 GLEISEINEDLKECFDDME 838

RESULT 7
Q98TR8 PRELIMINARY; PRT; 1466 AA.
AC Q98TR8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Bufo bufo (European toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Bufo.
OX NCBI_TaxID=8384;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BELLY SKIN;
RA Amstrup J., Hyild Larsen E.;
RT "Cloning of CFTR from Bufo bufo, Linnaeus, 1758."
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY026761; AAK07685.1; -.
DR EMBL: AY026761; AAK07685.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransportTM.
DR InterPro: IPR003439; ABC_transportr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR Pfam: PF00005; ABC_tran; 2.
DR ProDom: PD000006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 2.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1466 AA; 165997 MW; EB692EC3C611C169 CRC64;

Query Match          81.9%; Score 95; DB 13; Length 1466;
Best Local Similarity 85.7%; Pred. No. 6.3e-05;
Matches 18; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 LEISEINEDLKECFDDME 22
DB 812 LEISEINEDLKECFDDME 832

RESULT 8
P70034 PRELIMINARY; PRT; 1485 AA.
AC P70034;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator (Fragment).
GN CFTR.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96411723; PubMed=8810276;

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RA Price M.P., Ishihara H., Sheppard D.N., Welsh M.J.;
RT "Function of Xenopus cystic fibrosis transmembrane conductance
RT regulator (CFTR) Cl channels and use of human-Xenopus chimeras to
RT investigate the pore properties of CFTR."
RL J. Biol. Chem. 271:25184-25191(1996).
DR EMBL: U60209; AAC60023.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransprtTM.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR005291; CAMP_cl_Channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR PRODOM: PD00006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 2.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
FT NON_TER
SQ SEQUENCE 1485 AA; 168502 MW; 0BEAF0D2264D5A24 CRC64;

Query Match 78.4%; Score 91; DB 13; Length 1485;
Best Local Similarity 76.2%; Pred. No. 0.00023;
Matches 16; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 LEISEINEEDLKECFDDME 22
DB 820 LESEDIENEEDLKECFDDTD 840

RESULT 9

ID 073677 PRELIMINARY; PRT: 1503 AA.
AC 073677;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CFTR.
OS Fundulus heteroclitus (Killifish) (Mummichog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Atherinomorpha;
OC Cyprinodontiformes; Fundulidae; Fundulus.
CX NCBI_TaxID=8078;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98191134; PubMed=9530103;
RA Singer T.D., Tucker S.J., Marshall W.S., Higgins C.F.;
RT "A divergent CFTR homologue: highly regulated salt transport in the
RT euryhaline teleost F. heteroclitus";
RL Am. J. Physiol. 274:C715-C723(1998).
DR EMBL: AF000271; AAC41271.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR001140; ABCtransprtTM.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR005291; CAMP_cl_Channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR PRODOM: PD00006; ABC_transportr; 2.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW Transmembrane.
SQ SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;

Query Match 66.4%; Score 77; DB 13; Length 1503;
Best Local Similarity 65.0%; Pred. No. 0.023;
Matches 13; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 3 EISEINEEDLKECFDDME 22
:||||:||||:|||||

DB 831 DISEVDEDEMECFADRE 850

RESULT 10

ID 08SPT1 PRELIMINARY; PRT: 235 AA.
AC 08SPT1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulatory domain
DE (Fragment).
GN CFTR.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
CX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Yin H., Chen Y., Alendberg G., Reuss L.;
RT "CFTR-R domain sequence from chimpanzee genomic DNA."
RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF490140; AAM08348.1; -.
KW Transmembrane.
FT NON_TER
FT NON_TER
SQ SEQUENCE 235 AA; 26727 MW; 1257A413EBA9DCEF CRC64;

Query Match 58.6%; Score 68; DB 6; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GLEISEINEEDLK 14
DB 222 GLEISEINEEDLK 235

RESULT 11

ID 09IAR8 PRELIMINARY; PRT: 1518 AA.
AC 09IAR8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator II.
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
CX NCBI_TaxID=8030;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396404; PubMed=11504857;
RA Chen J.M., Cutler C., Jacques C., Boeuf G., Denamur E., Lecointre G.,
RA Mercier B., Gramb G., Ferec C.;
RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance
RT Regulator: Implications for Structure and Disease Models";
RL Mol. Biol. Evol. 18:1771-1788(2001).
DR EMBL: AF161070; AAF37801.1; -.
DR HSSP: P13569; INBD.
DR InterPro: IPR003593; AAA_ATPase.
DR InterPro: IPR001140; ABCtransprtTM.
DR InterPro: IPR003439; ABC_transport.
DR InterPro: IPR005291; CAMP_cl_Channel.
DR Pfam: PF00664; ABC_membrane; 2.
DR PRODOM: PD00006; ABC_transportr; 2.
DR SMART: SM00382; AAA; 1.
DR TIGRFAMS: TIGR00953; 3a01202; 1.
DR TIGRFAMS: TIGR01271; CFTR_protein; 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW ATP-binding; Transmembrane.
SQ SEQUENCE 1518 AA; 171136 MW; B3579B15820BA7F4 CRC64;

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RL Mol. Biol. Evol. 18:1771-1788(2001).
DR EMBL: AF155237; AAD38404.1; -
DR HSSP: P13369; 1MD.
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR001140; ABCtransp1TM.
DR InterPro: IPR003439; ABC_transpstr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane. 2.
DR Pfam: PF00005; ABC_tran. 2
DR ProDom: PD000006; ABC_transpstr. 2.
DR SMART: SM00382; AAA. 1.
DR TIGRfams: TIGR00953; 3a01202; 1.
DR TIGRfams: TIGR01271; CSTR_protein. 1.
DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
DR APF-binding; Transmembrane.
DR SEQUENCE 1519 AA; 171239 MM; F4A67DE22898240C CRC64;
SQ

Query Match 55.2%; Score 64; DB 13; Length 1519;
Best Local Similarity 45.0%; Pred. No. 1.6;
Matches 9; Conservative 9; Mismatches 2; Indels 0; Gaps 0;

OY 3 EISEINEDLKCEFPDME 22
Db 848 DISEVDQDMQCFADERE 867

RESULT 14
O91BE2 PRELIMINARY; PRT; 1511 AA.
AC O91BE2.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator.
GN CSTR.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorphi; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP MEDLINE FROM N.A.
RX MEDLINE=20414757; Pubmed=10956637;
RA Davidson H., Taylor W.S., Doherty A., Boyd A.C., Porteous D.J.;
RT "Genomic sequence analysis for Fugu rubripes CSTR and flanking genes in
RT a 60 kb region conserving synteny with 800 kb of human chromosome 7.";
RL Genome Res. 10:1194-1203(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Ayele K., Beckstrom-Sternberg S.M., Benjamin B., Blakesley R.W.,
RA Bouffard G.G., Brinley C., Brooks S., Dietrich N.L., Granite S.,
RA Guan X., Gupta J., Ho S.-L., Idol J.R., Karlins E., Lee-Lin S.-O.,
RA Legaspi R., Lim M., Maduro Q.L., Maduro V.B., Mastaglio C.,
RA Matrinan S.D., McCloskey J.C., McDowell J., Pearson R., Prasad A.,
RA Shavchenko Y., Snyder B., Staliridop S., Thomas J.W., Thomas P.J.,
RA Tjongson E.E., Touchman J.W., Tsirigos C., Vogt J.L., Walker M.A.,
RA Wehderby K.D., Zhang L.-H., Green E.D.;
RT "NISC Comparative Sequencing Initiative.";
RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ271361; CAB96905.1; -
DR EMBL: AC087333; AAL40378.1; -.
DR HSSP: P13369; 1MD.
DR InterPro: IPR003593; AAA_Atpase.
DR InterPro: IPR001140; ABCtransp1TM.
DR InterPro: IPR003439; ABC_transpstr.
DR InterPro: IPR005291; CAMP_cl_channel.
DR Pfam: PF00664; ABC_membrane. 2.
DR Pfam: PF00005; ABC_tran. 2.
DR ProDom: PD000006; ABC_transpstr. 2.
DR SMART: SM00382; AAA. 1.
DR TIGRfams: TIGR00953; 3a01202; 1.
DR TIGRfams: TIGR01271; CSTR_protein. 1.

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DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.
 KW ATP-binding; Transmembrane.
 SQ SEQUENCE 1511 AA; 170019 MW; 20EC4AC0EA721BB2 CRC64;

Query Match 53.4%; Score 62; DB 13; Length 1511;
 Best Local Similarity 45.0%; Pred. No. 3;
 Matches 9; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

OY 3 EISEINEEDLKECFDWE 22
 :||||:|||||:
 DB 839 DISEDVTEDEMEQCFADRD 858

RESULT 15

O9DDK8 PRELIMINARY; PRT; 244 AA.
 AC O9DDK8:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cystic fibrosis transmembrane conductance regulator (Fragment).
 GN CFTR.
 OS Necturus maculosus (Mudpuppy) (Waterdog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidae; Proteidae; Necturus.
 OX NCBI_TaxID=42757;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GALL BLADDER;
 RA Burton B., Torres R.J., Hellmich H.L., Reuss L.;
 RT "Cystic fibrosis transmembrane conductance regulator from Necturus
 maculosus.";
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF318308; AAC34562.1; -.
 DR HSSP; P13569; INBD.
 KW Transmembrane.
 FT NON_TER 1
 FT NON_TER 244
 SO SEQUENCE 244 AA; 27813 MW; BABDEB8B8C2FD36A CRC64;

Query Match 48.3%; Score 56; DB 13; Length 244;
 Best Local Similarity 84.6%; Pred. No. 3.6;
 Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LEISEINEEDLK 14
 |||:|||||:
 DB 232 LEINEINEEDLR 244

Search completed: July 16, 2003, 14:03:06
 Job time : 79 secs

